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#4

SEQUENCE LISTING

<110> Bartlett, Perry Francis
Coulson, Elizabeth Jane
Fieldew, Katrina
Baca, Manuel
Kilpatrick, Trevor
Surindar, Cheema

<120> Method of Modulating Cell Survival and
Reagents Useful for Same

<130> 3206.1001-000

<140> US 09/821,831

<141> 2001-03-30

<150> PCT/AU99/00860

<151> 1999-10-05

<150> AU PQ0701

<151> 1999-06-01

<150> AU PP6351

<151> 1998-10-07

<150> AU PP6353

<151> 1998-10-06

<160> 72

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<210> 1

<211> 3260

<212> DNA

<213> Artificial Sequence

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<223> Synthetic CDNA Sequence of Human

<221> CDS

<222> (115)...(1389)

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Met
1

agg agg gca ggt gct gcc tgc agc gcc atg gac cgg ctg cgc ctg ctg 165
Arg Arg Ala Gly Ala Ala Cys Ser Ala Met Asp Arg Leu Arg Leu Leu
5 10 15

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ctg ctg ctg att cta ggg gtg tcc tct gga ggt gcc aag gag aca tgt	213
Leu Leu Leu Ile Leu Gly Val Ser Ser Gly Gly Ala Lys Glu Thr Cys	
20 25 30	
tcc aca ggc ctg tac acc cac agc gga gag tgc tgc aaa gcc tgc aac	261
Ser Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn	
35 40 45	
ttg ggc gaa ggc gtg gcc cag ccc tgc gga gcc aac cag acc gtg tgt	309
Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys	
50 55 60 65	
gaa ccc tgc ctg gac aat gtt aca ttc tcc gat gtg gtg agc gcc act	357
Glu Pro Cys Leu Asp Asn Val Thr Phe Ser Asp Val Val Ser Ala Thr	
70 75 80	
gag ccg tgc aag ccg tgc acc gag tgc ctg ggc ctg cag agc atg tcc	405
Glu Pro Cys Lys Pro Cys Thr Glu Cys Leu Gly Leu Gln Ser Met Ser	
85 90 95	
gct ccc tgt gtg gag gca gac gat gca gtg tgc aga tgt gcc tat ggc	453
Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly	
100 105 110	
tac tac cag gac gag gag act ggc cac tgt gag gct tgc agc gtg tgc	501
Tyr Tyr Gln Asp Glu Glu Thr Gly His Cys Glu Ala Cys Ser Val Cys	
115 120 125	
gag gtg ggc tgc gga ctc gtg ttc tcc tgc cag gac aaa cag aac aca	549
Glu Val Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr	
130 135 140 145	
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Val Cys Glu Glu Cys Pro Glu Gly Thr Tyr Ser Asp Glu Ala Asn His	
150 155 160	
gtg gac ccg tgc cta ccc tgc acg gtg tgc gag gac act gag cgc cag	645
Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln	
165 170 175	
tta cgc gag tgc acg ccc tgg gct gat gct gaa tgc gaa gag atc cct	693
Leu Arg Glu Cys Thr Pro Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro	
180 185 190	
ggg cga tgg atc cca agg tct acg ccc ccg gag ggc tcc gac agc aca	741
Gly Arg Trp Ile Pro Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr	
195 200 205	
gcg ccc agc acc cag gag cct gag gtt cct cca gag caa gac ctt gta	789
Ala Pro Ser Thr Gln Glu Pro Glu Val Pro Pro Glu Gln Asp Leu Val	
210 215 220 225	
ccc agt aca gtg gcg gat atg gtg acc act gtg atg ggc agc tcc cag	837
Pro Ser Thr Val Ala Asp Met Val Thr Thr Val Met Gly Ser Ser Gln	
230 235 240	
cct gta gtg acc cgc ggc acc acc gac aac ctc att cct gtc tat tgc	885
Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys	
245 250 255	

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Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe	
260 265 270	
aag agg tgg aac agc tgc aaa caa aat aaa caa ggc gcc aac agc cgc	981
Lys Arg Trp Asn Ser Cys Lys Gln Asn Lys Gln Gly Ala Asn Ser Arg	
275 280 285	
ccc gtg aac cag acg ccc cca ccg gag gga gag aaa ctg cac agc gac	1029
Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp	
290 295 300 305	
agt ggc atc tct gtg gac agc cag agc ctg cac gac cag cag acc cat	1077
Ser Gly Ile Ser Val Asp Ser Gln Ser Leu His Asp Gln Gln Thr His	
310 315 320	
acg cag act gcc tca ggc cag gcc ctc aag ggt gat ggc aac ctc tac	1125
Thr Gln Thr Ala Ser Gly Gln Ala Leu Lys Gly Asp Gly Asn Leu Tyr	
325 330 335	
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Ser Ser Leu Pro Leu Thr Lys Arg Glu Glu Val Glu Lys Leu Leu Asn	
340 345 350	
ggg gat acc tgg cga cat ctg gca ggc gag ctg ggt tac cag cct gaa	1221
Gly Asp Thr Trp Arg His Leu Ala Gly Glu Leu Gly Tyr Gln Pro Glu	
355 360 365	
cat ata gac tcc ttt acc cac gag gcc tgc cca gtg cga gcc ctg ctg	1269
His Ile Asp Ser Phe Thr His Glu Ala Cys Pro Val Arg Ala Leu Leu	
370 375 380 385	
gcc agc tgg ggt gcc cag gac agt gca acg ctt gat gcc ctt tta gcc	1317
Ala Ser Trp Gly Ala Gln Asp Ser Ala Thr Leu Asp Ala Leu Leu Ala	
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gcc ctg cga cgc atc cag aga gct gac att gtg gag agt cta tgc agc	1365
Ala Leu Arg Arg Ile Gln Arg Ala Asp Ile Val Glu Ser Leu Cys Ser	
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Glu Ser Thr Ala Thr Ser Pro Val	
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gatatcttgc ttttctcccc atggctcttt tggggctgag actagatcct gctgggagtc 2439
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<211> 425

<212> PRT

<213> Artificial Sequence

<220>

<223> Deduced amino acid sequence

<400> 2

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          20          25          30
Cys Ser Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys
          35          40          45
Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val
          50          55          60
Cys Glu Pro Cys Leu Asp Asn Val Thr Phe Ser Asp Val Val Ser Ala
65          70          75          80
Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Leu Gly Leu Gln Ser Met
          85          90          95
Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr
          100          105          110
Gly Tyr Tyr Gln Asp Glu Glu Thr Gly His Cys Glu Ala Cys Ser Val
          115          120          125
Cys Glu Val Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn
          130          135          140
Thr Val Cys Glu Glu Cys Pro Glu Gly Thr Tyr Ser Asp Glu Ala Asn
145          150          155          160
His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg
          165          170          175
Gln Leu Arg Glu Cys Thr Pro Trp Ala Asp Ala Glu Cys Glu Glu Ile
          180          185          190
Pro Gly Arg Trp Ile Pro Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser
          195          200          205
Thr Ala Pro Ser Thr Gln Glu Pro Glu Val Pro Pro Glu Gln Asp Leu
          210          215          220
Val Pro Ser Thr Val Ala Asp Met Val Thr Thr Val Met Gly Ser Ser
225          230          235          240
Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr
          245          250          255
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Cys	Ser	Ile	Leu	Ala	Ala	Val	Val	Val	Gly	Leu	Val	Ala	Tyr	Ile	Ala
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Phe	Lys	Arg	Trp	Asn	Ser	Cys	Lys	Gln	Asn	Lys	Gln	Gly	Ala	Asn	Ser
		275					280					285			
Arg	Pro	Val	Asn	Gln	Thr	Pro	Pro	Pro	Glu	Gly	Glu	Lys	Leu	His	Ser
	290					295					300				
Asp	Ser	Gly	Ile	Ser	Val	Asp	Ser	Gln	Ser	Leu	His	Asp	Gln	Gln	Thr
305					310					315					320
His	Thr	Gln	Thr	Ala	Ser	Gly	Gln	Ala	Leu	Lys	Gly	Asp	Gly	Asn	Leu
				325				330						335	
Tyr	Ser	Ser	Leu	Pro	Leu	Thr	Lys	Arg	Glu	Glu	Val	Glu	Lys	Leu	Leu
			340				345					350			
Asn	Gly	Asp	Thr	Trp	Arg	His	Leu	Ala	Gly	Glu	Leu	Gly	Tyr	Gln	Pro
	355					360					365				
Glu	His	Ile	Asp	Ser	Phe	Thr	His	Glu	Ala	Cys	Pro	Val	Arg	Ala	Leu
	370					375				380					
Leu	Ala	Ser	Trp	Gly	Ala	Gln	Asp	Ser	Ala	Thr	Leu	Asp	Ala	Leu	Leu
385					390				395						400
Ala	Ala	Leu	Arg	Arg	Ile	Gln	Arg	Ala	Asp	Ile	Val	Glu	Ser	Leu	Cys
			405					410						415	
Ser	Glu	Ser	Thr	Ala	Thr	Ser	Pro	Val							
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<210> 3

<211> 867

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic CDNA sequence of rat

<221> CDS

<222> (115)...(867)

<400> 3

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					Met	
					1	

agg	agg	gca	ggt	gct	gcc	tgc	agc	gcc	atg	gac	cgg	ctg	cgc	ctg	ctg	165
Arg	Arg	Ala	Gly	Ala	Ala	Cys	Ser	Ala	Met	Asp	Arg	Leu	Arg	Leu	Leu	
		5						10				15				

ctg	ctg	ctg	att	cta	ggg	gtg	tcc	tct	gga	ggt	gcc	aag	gag	aca	tgt	213
Leu	Leu	Leu	Ile	Leu	Gly	Val	Ser	Ser	Gly	Gly	Ala	Lys	Glu	Thr	Cys	
		20					25				30					

tcc	aca	ggc	ctg	tac	acc	cac	agc	gga	gag	tgc	tgc	aaa	gcc	tgc	aac	261
Ser	Thr	Gly	Leu	Tyr	Thr	His	Ser	Gly	Glu	Cys	Cys	Lys	Ala	Cys	Asn	
	35					40				45						

ttg	ggc	gaa	ggc	gtg	gcc	cag	ccc	tgc	gga	gcc	aac	cag	acc	gtg	tgt	309
Leu	Gly	Glu	Gly	Val	Ala	Gln	Pro	Cys	Gly	Ala	Asn	Gln	Thr	Val	Cys	
	50				55				60						65	

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gaa ccc tgc ctg gac aat gtt aca ttc tcc gat gtg gtg agc gcc act	357
Glu Pro Cys Leu Asp Asn Val Thr Phe Ser Asp Val Val Ser Ala Thr	
70 75 80	
gag ccg tgc aag ccg tgc acc gag tgc ctg ggc ctg cag agc atg tcc	405
Glu Pro Cys Lys Pro Cys Thr Glu Cys Leu Gly Leu Gln Ser Met Ser	
85 90 95	
gct ccc tgt gtg gag gca gac gat gca gtg tgc aga tgt gcc tat ggc	453
Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly	
100 105 110	
tac tac cag gac gag gag act ggc cac tgt gag gct tgc agc gtg tgc	501
Tyr Tyr Gln Asp Glu Glu Thr Gly His Cys Glu Ala Cys Ser Val Cys	
115 120 125	
gag gtg ggc tgc gga ctc gtg ttc tcc tgc cag gac aaa cag aac aca	549
Glu Val Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr	
130 135 140 145	
gtg tgt gaa gag tgc cca gag ggc aca tac tca gac gaa gcc aac cac	597
Val Cys Glu Glu Cys Pro Glu Gly Thr Tyr Ser Asp Glu Ala Asn His	
150 155 160	
gtg gac ccg tgc cta ccc tgc acg gtg tgc gag gac act gag cgc cag	645
Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln	
165 170 175	
tta cgc gag tgc acg ccc tgg gct gat gct gaa tgc gaa gag atc cct	693
Leu Arg Glu Cys Thr Pro Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro	
180 185 190	
ggt cga tgg atc cca agg tct acg ccc ccg gag ggc tcc gac agc aca	741
Gly Arg Trp Ile Pro Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr	
195 200 205	
gcg ccc agc acc cag gag cct gag gtt cct cca gag caa gac ctt gta	789
Ala Pro Ser Thr Gln Glu Pro Glu Val Pro Pro Glu Gln Asp Leu Val	
210 215 220 225	
ccc agt aca gtg gcg gat atg gtg acc act gtg atg ggc agc tcc cag	837
Pro Ser Thr Val Ala Asp Met Val Thr Thr Val Met Gly Ser Ser Gln	
230 235 240	
cct gta gtg acc cgc ggc acc acc gac aac	867
Pro Val Val Thr Arg Gly Thr Thr Asp Asn	
245 250	

<210> 4

<211> 251

<212> PRT

<213> Artificial Sequence

<220>

<223> Deduced amino acid sequence

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 20          25          30
Cys Ser Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys
 35          40          45
Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val
 50          55          60
Cys Glu Pro Cys Leu Asp Asn Val Thr Phe Ser Asp Val Val Ser Ala
 65          70          75          80
Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Leu Gly Leu Gln Ser Met
 85          90          95
Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr
100          105          110
Gly Tyr Tyr Gln Asp Glu Glu Thr Gly His Cys Glu Ala Cys Ser Val
115          120          125
Cys Glu Val Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn
130          135          140
Thr Val Cys Glu Glu Cys Pro Glu Gly Thr Tyr Ser Asp Glu Ala Asn
145          150          155          160
His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg
165          170          175
Gln Leu Arg Glu Cys Thr Pro Trp Ala Asp Ala Glu Cys Glu Glu Ile
180          185          190
Pro Gly Arg Trp Ile Pro Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser
195          200          205
Thr Ala Pro Ser Thr Gln Glu Pro Glu Val Pro Pro Glu Gln Asp Leu
210          215          220
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225          230          235          240
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<210> 5
<211> 66
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic Oligonucleotide

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<221> CDS
<222> (1)...(66)

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gtg gcc tat att gct ttc
Val Ala Tyr Ile Ala Phe
20

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<210> 6
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Deduced amino acid sequence

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1 5 10 15
Ala Tyr Ile Ala Phe
20

<210> 7
<211> 105
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotides

<400> 7
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acgccccac cggagggaga gaaactgcac agcgacagtg gcatc 105

<210> 8
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Deduced amino acid sequence

<400> 8
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Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp
20 25 30
Ser Gly Ile
35

<210> 9
<211> 2222
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic

<221> CDS
<222> (1)...(351)
<223> Deduced amino acid sequence

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<400> 9

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gcc tca ggc cag gcc ctg aag ggt gat ggc aac ctg tac agt agc ctg 96
Ala Ser Gly Gln Ala Leu Lys Gly Asp Gly Asn Leu Tyr Ser Ser Leu
20 25 30

ccc ctg acc aag cgt gag gag gta gag aaa ctg ctg aac ggg gat acc 144
Pro Leu Thr Lys Arg Glu Glu Val Glu Lys Leu Leu Asn Gly Asp Thr
35 40 45

tgg cga cat ctg gca ggc gag ctg ggt tac cag cct gaa cat ata gac 192
Trp Arg His Leu Ala Gly Glu Leu Gly Tyr Gln Pro Glu His Ile Asp
50 55 60

tcc ttt acc cac gag gcc tgc cca gtg cga gcc ctg ctg gcc agc tgg 240
Ser Phe Thr His Glu Ala Cys Pro Val Arg Ala Leu Leu Ala Ser Trp
65 70 75 80

ggt gcc cag gac agt gca acg ctt gat gcc ctt tta gcc gcc ctg cga 288
Gly Ala Gln Asp Ser Ala Thr Leu Asp Ala Leu Leu Ala Ala Leu Arg
85 90 95

cgc atc cag aga gct gac att gtg gag agt cta tgc agc gag tcc act 336
Arg Ile Gln Arg Ala Asp Ile Val Glu Ser Leu Cys Ser Glu Ser Thr
100 105 110

gcc aca tcc cca gtg tgaactcaca gactgggagc ccctgtcctg tcccacattc 391
Ala Thr Ser Pro Val
115

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caagttggaa cctctggccc tccagctggt gactatgaac tccagacccc ttcgtgctcc 2131
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<210> 10

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Deduced amino acid sequence

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Pro Leu Thr Lys Arg Glu Glu Val Glu Lys Leu Leu Asn Gly Asp Thr
          35          40          45
Trp Arg His Leu Ala Gly Glu Leu Gly Tyr Gln Pro Glu His Ile Asp
          50          55          60
Ser Phe Thr His Glu Ala Cys Pro Val Arg Ala Leu Leu Ala Ser Trp
          65          70          75          80
Gly Ala Gln Asp Ser Ala Thr Leu Asp Ala Leu Leu Ala Ala Leu Arg
          85          90          95
Arg Ile Gln Arg Ala Asp Ile Val Glu Ser Leu Cys Ser Glu Ser Thr
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Ala Thr Ser Pro Val
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<222> (1)...(87)

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 1          5          10          15

ccc gtg aac cag acg ccc cca ccg gag gga gag aaa ctg 87
Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu
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58
11/26

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<220>
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20 25

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1 5 10 15
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20 25 30
Ser Gly

<210> 14
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<220>
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Lys Arg Trp Asn Ser Cys Lys Gln Asn Lys Gln Gly Ala Asn Ser Arg
1 5 10 15
Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp
20 25 30
Ser

<210> 15
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59
32/26

<400> 15
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20 25 30

<210> 16
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<220>
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20 25 30

<210> 17
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1 5 10 15
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20 25 30

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60
12/26

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<220>
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<400> 19
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20 25

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61
~~14/26~~

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1 5 10 15
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<400> 28
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1 5 10 15
Pro Val Asn

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1 5 10 15
Pro Val

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<400> 30
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63
~~16/26~~

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<210> 32
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65
~~18/26~~

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66
19/26

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<220>
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20 25 30
Gly Ile

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Trp Asn Ser Cys Lys Gln Asn Lys Gln Gly Ala Asn Ser Arg Pro Val
1 5 10 15
Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp Ser Gly
20 25 30
Ile

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1 5 10 15
Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp Ser Gly Ile
20 25 30

67
20/26

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20 25 30

<210> 47
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Cys Lys Gln Asn Lys Gln Gly Ala Asn Ser Arg Pro Val Asn Gln Thr
1 5 10 15
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20 25 30

<210> 48
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<212> PRT
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<220>
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Pro Pro Glu Gly Glu Lys Leu His Ser Asp Ser Gly Ile
20 25

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20 25

68
21/26

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20 25

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1 5 10 15
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20 25

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20 25

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69
22/26

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<220>
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<400> 54
Ala Asn Ser Arg Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys
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<400> 55
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His Ser Asp Ser Gly Ile
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<220>
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<400> 56
Ser Arg Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His
1 5 10 15
Ser Asp Ser Gly Ile
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<220>
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<400> 57
Arg Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser
1 5 10 15
Asp Ser Gly Ile
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70
~~23/26~~

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<400> 58
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1 5 10 15
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<400> 59
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1 5 10 15
Gly Ile

<210> 60
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<400> 60
Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp Ser Gly
1 5 10 15
Ile

<210> 61
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<212> PRT
<213> Artificial Sequence

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<400> 61
Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp Ser Gly Ile
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71
24/26

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<211> 15
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<220>
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<400> 62
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1 5 10 15

<210> 63
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1 5 10

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1 5 10

72
~~25/26~~

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<220>
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1 5 10

<210> 67
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<400> 67
Gly Glu Lys Leu His Ser Asp Ser Gly Ile
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